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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: THE SCRIPPS RESEARCH INSTITUTE
- (B) STREET: 10550 North Torrey Pines Road
- (C) CITY: La Jolla
- (D) STATE: California
- (E) COUNTRY: US
- (F) ZIP: 92037
- (G) TELEPHONE: (619) 784-2937
- (H) TELEFAX: (619) 784-9399

(ii) TITLE OF INVENTION: MHC CLASS II ANTIGEN PRESENTING SYSTEMS
AND METHODS FOR ACTIVATING CD4+ T CELLS

(iii) NUMBER OF SEQUENCES: 56

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/
- (B) FILING DATE: 22-MAY-1997
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/018,175
- (B) FILING DATE: 23-MAY-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTCGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAACTTCCA TGAAAATAT	60
GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC TTAATTAAAA	120
TAGATAAATG GGAGCGGCTG GAATGGCGGA GCATGACCAA GTTCCCTCCGC CAATCAGTCG	180
TAAAACAGAA GTCGTGGAAA GCGGATAGAA AGAATGTTCG ATTTGACGGG CAAGCATGTC	240
TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT CATGACCAAG	300
AATATAGCGG TGTGAGTGAG CGGGAAGCTC GGTTTCTGTC CAGATCGAAC TCAAAACTAG	360
TCCAGCCAGT CGCTGTCGAA ACTAATTAAG TTAATGAGTT TTTCATGTTA GTTTCGGCT	420
GAGCAACAAT TAAGTTTATG TTTCAGTTCC GCTTAGATTT CGCTGAAGGA CTTGCCACTT	480
TCAATCAATA CTTTAGAACAA AAATCAAAAC TCATTCTAAT AGCTTGGTGT TCATCTTTT	540
TTTTAATGAT AAGCATTTCG TCGTTTATAC TTTTTATATT TCGATATTAA ACCACCTATG	600
AAGTTCAATT TAATCGCCAG ATAAGCAATA TATTGTGTAATATTTGTAT TCTTTATCAG	660
GAAATTCAAGG GAGACGGGGA AGTTACTATC TACTAAAAGC CAAACAATT CTTACAGTT	720
TACTCTCTCT ACTCTAGAGT	740

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGTTGC AGGACAGGAT GTGGTGCCCCG ATGTGACTAG CTCTTGCTG CAGGCCGTCC	60
TATCCTCTGG TTCCGATAAG AGACCCAGAA CTCCGGCCCC CCACCGCCCA CCGCCACCCC	120

CATACATATG TGGTACGCAA GTAAGAGTGC CTGCCATGC CCCATGTGCC CCACCAAGAG	180
TTTGCATCC CATAAAAGTC CCCAAAGTGG AGAACCGAAC CAATTCTTCG CGGGCAGAAC	240
AAAAGCTTCT GCACACGTCT CCACTCGAAT TTGGAGCCGG CCGGCGTGTG CAAAAGAGGT	300
GAATCGAACG AAAGACCCGT GTGTAAAGCC GCGTTCCAA AATGTATAAA ACCGAGAGCA	360
TCTGGCCAAT GTGCATCAGT TGTGGTCAGC AGCAAAATCA AGTGAATCAT CTCAGTGCAA	420
CTAAAGG	427

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGAATTCC ACCATGCCGT GCAGCAGAGC TCTGA

35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTGGATCCT CATAAAGGCC CTGGGTGTC

29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTGAATTCC ACCATGGCTC TGCAGATCCC CA

32

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGGATCCT CACTGCAGGA GCCCTGCT

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGTTGCAGG ACAGGGATGTG GTGCCCGATG TGACTAGCTC TTTGCTGCAG GCCGTCTTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCC ACGCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCC ATGTGCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTG GAGCGGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCCGG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTCAAGCAG AAAATCAAGT GAATCATCTC AGTCAACTA	420
AAGGGGGGAA TTCCTGCAGA GACCTCCCAG AGACCAGGAT GCCGTGCAGC AGAGCTCTGA	480
TTCTGGGGGT CCTCGCCCTG AACACCATGC TCAGCCTCTG CGGAGGTGAA GACGACATTG	540
AGGCCGACCA CGTAGGCTTC TATGGTACAA CTGTTATCA GTCTCCTGGA GACATTGGCC	600
AGTACACACA TGAATTGAT GGTGATGAGT TGTCTATGT GGACTTGGAT AAGAAGAAAA	660
CTGTCTGGAG GCTTCCTGAG TTTGGCAAT TGATACTCTT TGAGCCCCAA GGTGGACTGC	720
AAAACATAGC TGCAGAAAAA CACAACTTGG GAATCTTGAC TAAGAGGTCA AATTCACCC	780
CAGCTACCAA TGAGGCTCCT CAAGCGACTG TGTTCCCCAA GTCCCTGTG CTGCTGGTC	840
AGCCCAACAC CCTTATCTGC TTTGTGGACA ACATCTCCC ACCTGTGATC AACATCACAT	900
GGCTCAGGAA TAGCAAGTCA GTCACAGACCG GCGTTTATGA GACCAGCTTC CTCGTCAACC	960
GTGACCATTG CTTCCACAAG CTGTCTTATC TCACCTTCAT CCCCTCTGAT GATGACATTT	1020
ATGACTGCAA GGTGGAGCAC TGGGGCCTGG AGGAGCCGGT TCTGAAACAC TGGGAACCTG	1080
AGATTCCAGC CCCCATGTCA GAGCTGACAG AAACGTGGT GTGTGCCCTG GGGTTGTCTG	1140
TGGGCCTTGT GGGCATCGTG GTGGGCACCA TCTTCATCAT TCAAGGCCTG CGATCAGGTG	1200
GCACCTCCAG ACACCCAGGG CCTTTATGAG TCACACCTG GAAAGGAAGG TGTGTGTCCC	1260
TCTTCATGGA AGAAGTGGTG TTCTGGGTGT CGAATTGAG CTCGGTACCC GGGGATCCTC	1320
TAGAGTCGAC CTGCAGGCAT GCAATTGAT GCACACTCAC ATTCTTCTCC TAATACGATA	1380
ATAAAACCTT CCATGAAAAA TATGGAAAAA TATATGAAAA TTGAGAAATC CAAAAAAACTG	1440
ATAAACGCTC TACTTAATTA AAATAGATAA ATGGGAGCGG CAGGAATGGC GGAGCATGGC	1500
CAAAGTTCCTC CGCCAATCAG TCGTAAAACA GAAGTCGTGG AAAGCGGATA GAAAGAATGT	1560
TCGATTTGAC GGGCAAGCAT GTCTGCTATG TGGCGGATTG CGGAGGAATT GCACTGGAGA	1620
CCAGCAAGGT TCTCATGACC AAGAATATAG CGGTGAGTGA GCGGGAAGCT CGGTTCTGT	1680
CCAGATCGAA CTCAAAACCA GTCCAGCCAG TCGCTGTGAA AACTAATTAA GTAAATGAGT	1740

TTTCATGTT AGTTCGCC TGAGCAACAA TTAAGTTTAT GTTCAGTTC GGCTTAGATT	1800
TCGCTGAAGG ACTTGCCT TTCAATCAAT ACCTTACAAC AAAATCAAAA CTCATTCTAA	1860
TAGCTTGGTG TTCATCTTT TTTTAATGA TAAGCATTGT GTCGTTATA CTCTTATAT	1920
TTCGATATTA AACCACCTAT GAAGTTCATT TTAATGCCA GATAAGGAAT ATATTGTGTA	1980
AATATTGTA TTCTTATCA GGAAATTCAAG GGAGACGGGG AAGTTACTAT CTACTAAAAG	2040
CCAAACAATT TCTTACAGTT TTACTCTCTC TACTCTAGAG CTTGGCACTG GCCGTCGTT	2100
TACAACGTCG TGACTGGAA AACCCCTGGCG TTACCCAACT TAATGCCCT GCAGCACATC	2160
CCCCTTCGC CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATGCCCT TCCCAACAGT	2220
TGGCAGCCT GAATGGCGAA TGGCGCCTGA TGCGGTATTT TCTCCTTACG CATCTGTGCG	2280
GTATTCACA CCGCATATGG TGCCTCTCA GTACAATCTG CTCTGATGCC GCATAGTTAA	2340
GCCAGCCCCG ACACCCGCCA ACACCCGCTG ACGGCCCTG ACGGGCTTGT CTGCTCCGG	2400
CATCCGCTTA CAGACAAGCT GTGACCGTCT CCGGGAGCTG CATGTGTCAG AGGTTTCAC	2460
CGTCATCACC GAAACCGCG AGACGAAAGG GCCTCGTAT ACCGCTATT TTATAGGTTA	2520
ATGTCTGAT AATAATGGTT TCTTAGACGT CAGGTGGCAC TTTTCGGGA AATGTGGCG	2580
GAACCCCTAT TTGTTTATTT TTCTAAATAC ATTCAAATAT GTATCCGCTC ATGAGACAAT	2640
AACCCGTATA AATGCTCAA TAATATTGAA AAAGGAAGAG TATGAGTATT CAACATTCC	2700
GTGTCGCCCT TATTCCCTT TTTGCGGCAT TTTGCCCTCC TGTTTTGCT CACCCAGAAA	2760
CGCTGGTGAAG AGTAAAAGAT GCTGAAGATC AGTTGGGTGC ACGAGTGGGT TACATCGAAC	2820
TGGATCTCAA CAGCGTAAG ATCCCTGAGA GTTTGCCCG CGAAGAACGT TTTCAATGA	2880
TGAGCACTTT TAAAGTTCTG CTATGTGGG CGGTATTATC CCGTATTGAC GCCGGGCAAG	2940
AGCAACTCGG TCGCCGCATA CACTATTCTC AGAATGACTT GGTTGAGTAC TCACCAAGTCA	3000
CAGAAAAGCA TCTTACGGAT GGCATGACAG TAAGAGAATT ATGCAGTGCT GCCATAACCA	3060
TGAGTGATAA CACTGCCGCC AACTTACTTC TGACAACGAT CGGAGGACCG AAGGAGCTAA	3120
CCGCTTTTT GCACAACATG GGGGATCATG TAACTGCCCT TGATCGTTGG GAACCGGAGC	3180
TGAATGAAGC CATAACAAAC GACCGAGCGTG ACACCACGAT GCCTGTAGCA ATGGCAACAA	3240
CGTTGCGCAA ACTATTAACG GCGGAACATAC TTACTCTAGC TTCCCGGCAA CAATTAATAG	3300
ACTGGATGGA GGCGGATAAA GTTGCAGGAC CACTCTGCG CTGGCCCTT CCGGCTGGCT	3360
GGTTTATTGC TGATAAAATCT GGAGCCGGTG AGCGTGGTC TCGGGTATC ATTGCAGCAC	3420
TGGGGCCAGA TGGTAAGCCC TCCCCTATCG TAGTTATCTA CACGACGGGG AGTCAGGCAA	3480
CTATGGATGA ACGAAATAGA CAGATCGCTG AGATAGGTGC CTCACTGATT AAGCATTGGT	3540
AACTGTAGA CCAAGTTTAC TCATATATAC TTTAGATTGA TTIAAAACTT CATTNTTAAT	3600
TTAAAAGGAT CTAGGTGAAG ATCCTTTTG ATAATCTCAT GACCAAAATC CCTTAAGGTG	3660
AGTTTCGTT CCACTGAGCG TCAGACCCCG TAGAAAAGAT CAAAGGATCT TCTTGAGATC	3720
CTTTTTCT CGCGTAATC TGCTGCTTGC AAACAAAAAA ACCACCGCTA CCAGCGGTGG	3780
TTTGTGCGGC GGATCAAGAG CTACCAACTC TTTTCCGAA GGTAACTGGC TTCAGCAGAG	3840
CGCAGATACC AAATACTGTC CTTCTAGTGT AGCCGTAGTT AGGCCACCCAC TTCAAGAACT	3900
CTGTAGCACC GCCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGCT GCTGCCAGTG	3960
GCGATAAGTC GTGTCTTACC GGGTTGGACT CAAGACGATA GTTACGGAT AAGGCGCAGC	4020
GGTCGGGCTG AACGGGGGGT TCGTGCACAC AGCCCAGCTT GGAGCGAACG ACCTACACCG	4080

AACTGAGATA CCTACAGCGT GAGCATTGAG AAAGCGCCAC GCTTCCCAGA GGGAGAAAGG	4140
CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA CGGCACGAGG GAGCTTCAG	4200
GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC	4260
GATTTTGTC ATGCTCGTCA GGGGGCCGGA GCCTATGGAA AAACGCCAGC AACGGCCCT	4320
TTTTACGGTT CCTGGCCTT TGCTGGCCTT TTGCTCACAT GTTCTTCCT GCGTTATCCC	4380
CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC	4440
GAACGACCGA CGCGAGCGAG TCAGTGAGCG AGGAAGCGGA AGAGGCCCA ATACGCAAAC	4500
CGCCTCTCCC CGCGCGTTGG CGGATTCAAT AATGCAGCTG GCACGACAGG TTTCCCGACT	4560
GGAAAGCGGG CAGTGAGCGC AACGCAATT AATGTGAGTTA GCTCACTCAT TAGGCACCCC	4620
AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAAAT	4680
TTCACACAGG AAACAGCTAT GACCATGATT ACG	4713

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTTGCAGG ACAGGATGTG GTGCCGATG TGACTAGCTC TTTGCTGCAG GCCGTCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCAGA CGGCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCG ATGTGCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGGGC GGAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTG GAGCCGGCCG CGGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGGG TTTCCAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTCAAGCAG AAAATCAAGT GAATCATCTC AGTGCACACTA	420
AAGGGGGGAA TTCCCTGCTG TGCCCTAGAG ATGGCTCTGC AGATCCCCAG CCTCCTCCTC	480
TCAGCTGCTG TGTTGGTGCT GATGGTGCTG AGCAGCCAG GGACTGAGGG CGGAAACTCC	540
GAAAGGCATT TCGTGGTCCA GTTCAAGGGC GAGTGCTACT ACACCAACGG GACGCAGCGC	600
ATACGGCTCG TGACCAAGATA CATCTACAAAC CGGGAGGAGT ACGTGCCTA CGACAGCGAC	660
GTGGCGAGT ACCGGCGGGT GACCGAGCTG GGGCGGCCAG ACGCCGAGTA CTGGAACAGC	720

CAGCCGGAGA	TCCTGGAGCG	AACGCCGCC	GAGGTGGACA	CGCGTGCAG	ACACAAC	TAC	780
GAGGGGCCGG	AGACCAGCAC	CTCCCTGCGG	CGGCTTGAAAC	AGCCCAATAT	CGCCATCTCC		840
CTGTCCAGGA	CAGAGGCCCT	CAACCACCAC	AAACACTCTGG	TCTGTTCGGT	GACAGATTTC		900
TACCCAGCCA	AGATCAAAGT	GGCCTGGTTC	AGGAATGGCC	AGGAGGAGAC	AGTGGGGTC		960
TCATCCACAC	AGCTTATTAG	GAATGGGGAC	TGGACCTTCC	AGGTCTGTT	CATGCTGGAG		1020
ATGACCCCCTC	ATCAGGGAGA	GGTCTACACC	TGCCATGTGG	AGCATCCCAG	CCTGAAGAGC		1080
CCCATCACTG	TGGAGTGGAG	GGCACAGTCC	GAGTCTGCC	GGAGCAAGAT	GTTGAGCGGC		1140
ATCGGGGGCT	GCCTGCTTGG	GGTGATCTTC	CTCGGGCTCG	GCCTTTCAT	CCGTCACAGG		1200
AGTCAGAAAAG	GACCTCGAGG	CCCTCCTCCA	GCAGGGCTCC	TGCAAGTGC	CAGAGTGT		1260
TGACTCAGTT	GACTGTCTCA	GACTGTAAGA	CCTACATGTC	TGCAATTGCA	GCTCGGTACC		1320
CGGGGATCCT	CTAGAGTCGA	CCTGCCAGGA	TGCAATTGCA	TGCAACTC	CATTCTCTC		1380
CTAATACGAT	AATAAAACTT	TCCATGAAAAA	ATATGAAAAA	ATATATGAAA	ATTGAGAAAT		1440
CCAAAAAAACT	GATAAACGCT	CTACTTAATT	AAAATAGATA	AATGGGAGCG	GCAGGAATGG		1500
CGGAGCATGG	CCAAGTTCCT	CCGCCAATCA	GTGCTAAAC	AGAAGTCGTG	GAAAGCGGAT		1560
AGAAAGAATG	TTCGATTG	CGGGCAAGCA	TGTCTGCTAT	GTGGCGGATT	CGGGAGGAAT		1620
TGCACTGGAG	ACCAGCAAGG	TTCTCATGAC	CAAGAATATA	CGGGTGAGTC	AGCGGGAAAGC		1680
TCGGTTTCTG	TCCAGATCGA	ACTCAAAACT	AGTCCAGCCA	GTGCGTGTG	AAACTAATTA		1740
AGTAAATGAG	TTTTCATGT	TAGTTCGCG	CTGAGCAACA	ATTAAGTTA	TGTTTCAGTT		1800
CGGCTTAGAT	TTCGCTGAAG	GACTGCCAC	TTTCAATCAA	TACTTTAGAA	CAAAATCAA		1860
ACTCATTCTA	ATAGCTTGGT	GTTCATCTT	TTTTTTAATG	ATAAGCATT	TGTCGTTTAT		1920
ACTTTTTATA	TTTCGATAATT	AAACCACCTA	TGAAGTTCAT	TTAATCGCC	AGATAAGCAA		1980
TATATTGTGT	AAATATTGT	ATTCTTTATC	AGGAAATTCA	GGGAGACGGG	GAAGTTACTA		2040
TCTACTAAAA	GCCAAACAAT	TTCTTACAGT	TTTACTCTCT	CTACTCTAGA	GCTTGGCACT		2100
GGCCGTCGTT	TTACAACGTC	GTGACTGGGA	AAACCCCTGGC	GTTACCCAAC	TTAATGCCCT		2160
TGCAGCACAT	CCCCCTTCG	CCAGCTGGCG	TAATAGCGAA	GAGGCCGCA	CCGATGCC		2220
TTCCCAACAG	TTGCCGAGCC	TGAATGGCGA	ATGGCCCTG	ATGCCGTATT	TTCTCCTTAC		2280
GCATCTGTG	GGTATTTCAC	ACCGCATATG	GTGCACTCTC	AGTACAATCT	GCTCTGATGC		2340
CGCATAGTTA	AGCCAGCCCC	GACACCCGCC	AACACCCGCT	GACGCGCC	GACGGGCTG		2400
TCTGCTCCCC	GCATCCGCTT	ACAGACAAGC	TGTGACCGTC	TCCGGGAGCT	GCATGTGTCA		2460
GAGGTTTTCA	CCGTCATCAC	CGAAACGCC	GAGACGAAAG	GGCCTCGTGA	TACGCCATT		2520
TTTATAGGTT	AATGTATG	TAATAATG	TTCTTAGACG	TCAGGTGGCA	CTTTTGGGG		2580
AAATGTGCGC	GGAAACCCCTA	TTTGTATT	TTTCTAAATA	CATTCAAATA	TGTATCCGCT		2640
CATGAGACAA	TAACCCGTAT	AAATGCTCA	ATAATATTGA	AAAAGGAAGA	GTATGACTAT		2700
TCAACATTTC	CGTGTGCC	TTATTCCCTT	TTTGGGCA	TTTGCCTTC	CTGTTTTGC		2760
TCACCCAGAA	ACGCTGGTGA	AAAGTAAAGA	TGCTGAAGAT	CAGTTGGGTG	CACGAGTGGG		2820
TTACATCGAA	CTGGATCTCA	ACAGCGTAA	GATCCTGAG	AGTTTCGCC	CCGAAGAACG		2880
TTTCTCAATG	ATGAGCACTT	TTAAAGTTCT	GCTATGTGGC	GCGGTATTAT	CCCGTATTGA		2940
CGCCGGGCAA	GAGCAACTCG	GTGCGCGCAT	ACACTATTCT	CAGAATGACT	TGGTTGAGTA		3000
CTCACCAAGTC	ACAGAAAAGC	ATCTTACGGA	TGGCATGACA	GTAAGAGAAAT	TATGCAGTGC		3060

TGCCATAACC ATGAGTGATA ACAC TGCGGC CAACTTACTT CTGACAACGA TCGGAGGACC	3120
GAAGGAGCTA ACCGCTTTT TGCACAACAT GGGGGATCAT GTAAC TCGCC TTGATCGTTG	3180
GGAACCGGAG CTGAATGAAG CCATACCAAA CGACGAGCGT GACACCACGA TGCCTGTAGC	3240
AATGGCAACA ACGTTGCGCA AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCC GGCA	3300
ACAATTAAATA GACTGGATGG AGGCGGATAA AGTTGCAGGA CCAC TTCTGC GCTCGGCCCT	3360
TCCGGCTGGC TGGTTTATTG CTGATAAAATC TGGAGCCGGT GACCGTGGGT CTCGGGTAT	3420
CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC GTAGTTATCT ACACGACGGG	3480
GAGTCAGGCA ACTATGGATG AACGAAATAG ACAGATCGCT GAGATAGGTG CCTCACTGAT	3540
TAAGCATTGG TAACTGTCA GACCAAGTTA CTCATATATA CTTTAGATTG ATTAAA ACT	3600
TCATTTTAA TTTAAAAGGA TCTAGGTGAA GATCCTTTT GATAATCTCA TGACCAAAAT	3660
CCCTTAACGT GAGTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC	3720
TTCTTGAGAT CCTTTTTTC TGCGCGTAAT CTGCTGTTG CAAACAAAAA AACCAACCGCT	3780
ACCAGCGGTG GTTTGTTGC CGGATCAAGA GCTACCAACT CTTTTCCGA AGGTAAC TGG	3840
CTTCAGCAGA GCGCAGATA CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA	3900
CTTCAAGAAC TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCA GTGGC	3960
TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA	4020
TAAGGCGCAG CGGTGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC	4080
GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCATTGA GAAAGCGCCA CGCTTCCGA	4140
AGGGAGAAAG GCGGACAGGT ATCCGTAAG CGGCAGGGTC GGAACAGGAG AGGGCACCGAG	4200
GGAGCTTCCA GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG	4260
ACTTGAGCGT CGATTTTGT GATGCTCGTC AGGGGGCGG AGCTATGGA AAAACGCCAG	4320
CAACCGGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTCC	4380
TGCGTTATCC CCTGATTCTG TGGATAACCG TATTACCGCC TTGAGTGAG CTGATAACCGC	4440
TCGCCGCAGC CGAACGACCG AGCCGAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC	4500
AATACGCAA CCGCCTCTCC CGCGCGTTG GCGGATT CAT TAATGCAGCT GGCACGACAG	4560
GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT AGCTCACTCA	4620
TTAGGCACCC CAGGCTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG	4680
CGGATAACAA TTTCACACAG GAAACAGCTA TGACCATGAT TACG	4724

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACCATGGC CATTAGTGG A GTC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGGATCCT TACAGAGGCC CCCTGCGTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACCATGGT GTGTCTGAGG CTCC

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTGGGATGCT CAGCTCAGGA ATCCTCTTG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCACCATGGT CCTAAACAAA GCTCTGAT

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGGATCCT CACAAGGGCC CTTGGTGTCT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCATGGC TTGGAAGAAG GCCTTT

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

100

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTAGATCTC AGTGCAGAAG CCCTTT

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACCATGGG CCCTGAAGAC AGAAT

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTGGATCCT CACAGGGTCC CCTGGCC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACCATGGT TCTGCAGGTT TCTGCG

26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGGATCCT TATGCAGATC CTCGTTGAA

29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGAATTCAC TAGAGGCTAG AGCCAT

26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGGATCCTC ACAGGGTGAC TTGACC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCTTGCAGG ACAGGATGTG GTGCCCGATG TGACTAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCCA CGGCCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCG ATGTGCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCCAATTG GAGCCCCCG GCGTGTGCAA AACAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTCAAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGAA TTCGATCTAG AGGCTAGAGC CATGGATGAC CAACCGCGACC TCATCTCTAA	480
CCATGAGCAA TTGCCCATAAC TGGCAACCG CCCTAGAGAG CCAGAAAGGT GCAGCCGTGG	540
AGCTCTGTAC ACCGGTGTGTT CTGTCCTGGT GGCTCTGCTC TTGGCTGGGC AGGCCACCAC	600
TGCTTACTTC CTGTACCAGC AACAGGGCCG CCTAGACAAG CTGACCATCA CCTCCCAGAA	660
CCTGCAACTG GAGAGCCTTC GCATGAAGCT TCCGAAATCT GCCAAACCTG TGAGCCAGAT	720
GCGGATGGCT ACTCCCTTGC TGATGCCATC AATGTCCATG GATAACATGC TCCTTGGGCC	780
TGTGAAGAAC GTTACCAAGT ACGGCAACAT GACCCAGGAC CATGTGATGC ATCTGCTCAC	840
GAGGTCTGGA CCCCTGGAGT ACCCGCAGCT GAAGGGGACC TTCCCAGAGA ATCTGAAGCA	900
TCTTAAGAAC TCCATGGATG GCGTGAACTG GAAGATCTTC GAGAGCTGGA TGAAGCAGTG	960
GCTCTTGTGTT GAGATGAGCA AGAACTCCCT GGAGGAGAAG AAGCCCACAG AGGCTCCACC	1020
TAAAGAGCCA CTGGACATGG AAGACCTATC TTCTGCCCTG GGAGTGACCA GGCAGGAAC	1080
GGGTCAAGTC ACCCTGTGAA GACAGAGGCC AGCATCAAGC TTATCGATAC CGTCGACCTG	1140
CAGGCATGCA ATTGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAACTTTCCA	1200
TGAAAAATAT GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC	1260
TTAATTAAAA TAGATAAAATG GGAGCGGCAG GAATGGCGGA GCATGGCCAA GTTCCTCCGC	1320
CAATCAGTCG TAAAACAGAA GTCGTGGAAA GCGGATAGAA AGAATGTTCG ATTTGACGGG	1380
CAAGCATGTC TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT	1440
CATGACCAAG AATATAGCGG TGAGTGAGCG GGAAGCTCGG TTTCTGTCCA GATCGAACTC	1500
AAAACTAGTC CAGCCAGTCG CTGTCGAAAC TAATTAAGTA AATGAGTTTT TCATGTTAGT	1560
TTCCGCGCTGA GCAACAATTA AGTTTATGTT TCAGTTGGC TTAGATTTCG CTGAAGGACT	1620
TGCCACTTTC AATCAATACT TTAGAACAAA ATCAAAACTC ATTCTAATAG CTTGGTGTTC	1680
ATCTTTTTT TTAATGATAA GCATTTGTC GTTTATACCTT TTTATATTTTC GATATTAAAC	1740
CACCTATGAA GTTCATTGAA ATGCCAGAT AAGCAATATA TTGTGTAAAT ATTTGTATTC	1800
TTTATCAGGA AATTCAAGGAA GACGGGGAAAG TTACTATCTA CTAAAAGCCA AACAAATTCT	1860
TACAGTTTA CTCTCTCTAC TCTAGAGCTT GGCACTGGCC GTCGTTTAC AACGTCGTGA	1920
CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG	1980
CTGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA	2040
TGGCGAATGG CGCCTGATGC GGTATTTCT CCTTACGGAT CTGTGCGGTA TTTCACACCG	2100

CATATGGTGC ACTCTCAGTA CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGCCCCGACA	2160
CCCGCCAACA CCCGCTGACG CGCCCTGACG GGCTTGTCTG CTCCCGGCAT CCGCTTACAG	2220
ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT GTGTCAGAGG TTTTCACCGT CATCACCGAA	2280
ACGCCGAGA CGAAAGGGCC TCGTGATAAC CCTATTGTTA TAGGTTAACAT TCATGATAAT	2340
AATGGTTTCT TAGACGTCAG GTGGCACTTT TCGGGGAAAT GTGCGCGGAA CCCCTATTG	2400
TTTATTTTTC TAAATACATT CAAATATGTA TCCGCTCATG AGACAATAAC CCTGATAAAAT	2460
GCTTCAATAA TATTGAAAAA GGAAGAGTAT GAGTATTCAA CATTTCCTGT TCGCCCTTAT	2520
TCCCTTTTTT GCGGCATTTT GCCTTCCTGT TTTTGCTCAC CCAGAAACGC TGGTGAAAGT	2580

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGAATTCAC CATGGATGAT CAGGGCGACC TT

32

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAAGGATCCT CACATGGGA CTGGGCCAG A

31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACCATGGG TCATGAACAG AACCA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGTGACT CAGTCACCTG AGCAAGG

27

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAACCATGGT CTCATTCCCTG CC

22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTGACCC TAGGAAATGT GCCATCC

27

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTAGAATTC ACCATGGCTT CAACCCGTGC CAAG

34

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTAGTCGAC TCAGGGAGGT GGGGCTTGTC C

31

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACCCCTTGAAT TCATGGCTCC CAGCAGCCCC CGGCC

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATTACCGGAT CCTCAGGGAG GCGTGGCTTG TGTGTTCGG

39

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGGTACCCG TGGAGACTGC CAGAGAT

27

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTGGATCCC TATGGCCGGA AGGCCTG

27

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAATTCCCT GTCAGAACATGG CCACCAT

27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTAGATCTT CACTCAGCTC TGGACGGT

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCCTTGAGC TCATGGTTGC TGGGAGCGAC GCGGGG

36

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATTACCGGAT CCTTAAAGAA CATTATATA CAGCACATA CA

42

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTAGAATT ACCATGGCTT GCAATTGTCA GTTG

34

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTAGTCGAC CTAAAGGAAG ACGGTCTGTT C

31

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCCCTTGAAT CCATGGGCCA CACACGGAGG CAG

33

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATTACCGGAT CCTTATACAG GGCGTACACT TTCCCTTCT

39

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTAGAATTG ACCATGGACC CCAGATGCAC CATGGG

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTTAGTCGAC TCACTCTGCA TTTGGTTTG CTGA

34

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCCTTGAGC TCATGGATCC CCAGTGCACT ATG

33

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTACCCCCG GGTTAAAAAC ATGTATCACT TTTGTCGCAT GA

42

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGGATCCA CCATGCAGCA GCCCTTCAAT T

31

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTGGATCCT TAGAGCTTAT ATAAGCCGA

29

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAAGAATTCTG GTACCATGCC GGAGGGAGGT TCGG

34

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTGGATCCT CAGGGCGCA CCCACTGCA

29

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly

1

5

10

15

Arg

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Thr Ile Ala Thr Asp Glu Glu Ala Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe Val Arg Phe Asp Ser Asp Ala Ala Ser Gln Arg Met
1 5 10